



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Linsley, Peter S.
Ledbetter, Jeffrey A.
Damle, Nitin K.
Brady, William
Wallace, Philip M.
- (ii) TITLE OF THE INVENTION: CTLA4/CD28Ig HYBRID FUSION
PROTEINS AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 22
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Mandel & Adriano
 - (B) STREET: 35 N. Arroyo Parkway, Suite 60
 - (C) CITY: Pasadena
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 91103
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/454,651
 - (B) FILING DATE: 06-DEC-1999
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/228,208
 - (B) FILING DATE: 15-APR-1994
 - (A) APPLICATION NUMBER: 08/008,898
 - (B) FILING DATE: 22-JAN-1993
 - (A) APPLICATION NUMBER: 07/723,617
 - (B) FILING DATE: 27-JUL-1991
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Adriano, Sarah B
 - (B) REGISTRATION NUMBER: 34,470
 - (C) REFERENCE/DOCKET NUMBER: 30436-30US01
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 310 445-1140
 - (B) TELEFAX: 310 445-9031
 - (C) TELEX:

- (2) INFORMATION FOR SEQ ID NO:1:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTAGCCACTG AAGCTTCACC ATGGGTGTAC TGCTCACAC

39

- (2) INFORMATION FOR SEQ ID NO:2:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGGCATGGGC TCCTGATCAG GCTTAGAAGG TCCGGGAAA

39

- (2) INFORMATION FOR SEQ ID NO:3:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTGGGCTCC TGATCAGGAA AATGCTCTTG CTTGGTTGT

39

- (2) INFORMATION FOR SEQ ID NO:4:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAGCAAGAGC ATTTTCCTGA TCAGGAGCCC AAATCTTCTG ACAAAACTCA CACATCCCCA

60

CCGTCCCCAG CACCTGAACT CCTG

84

- (2) INFORMATION FOR SEQ ID NO:5:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTCGACCAG TCTAGAAGCA TCCTCGTGCG ACCGCGAGAG C

41

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATTGCACAG TCAAGCTTCC ATGCCCATGG GTTCTCTGGC CACCTTG

47

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCCACAGTG CAGTGATCAT TTGGATCCTG GCATGTGAC

39

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCAGTCTGG TCCTTGCACT CCTGTTTCCA AGCATGGCGA GCATGGCAAT GCACGTGGCC

60

CAGCC

65

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTGGGCTCC TGATCAGAAT CTGGGCACGG TTG

33

- (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTAGCCACTG AAGCTTCACC AATGGGTGTA CTGCTCACAC AGAGGACGCT GCTCAGTCTG 60

GTCCTTGCAC TC 72

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCAATGCACG TGGCCCAGCC TGCTGTGGTA GTG 33

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGATGTAACA TGTCTAGATC AATTGATGGG AATAAAATAA GGCTG 45

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 nucleotides
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..561
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCA ATG CAC GTG GCC CAG CCT GCT GTG GTA CTG GCC AGC AGC CGA GGC 48

Ala Met His Val Ala Gln Pro Ala Val Leu Ala Ser Ser Arg Gly

1 5 10 15

ATC GCC AGC TTT GTG TGT GAG TAT GCA TCT CCA GGC AAA GCC ACT GAG 96

Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu

20 25 30

GTC CGG GTG ACA GTG CTT CGG CAG GCT GAC AGC CAG GTG ACT GAA GTC	144
Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val	
35 40 45	
TGT GCG GCA ACC TAC ATG ATG GGG AAT GAG TTG ACC TTC CTA GAT GAT	192
Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp	
50 55 60	
TCC ATC TGC ACG GGC ACC TCC AGT GGA AAT CAA GTG AAC CTC ACT ATC	240
Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile	
65 70 75 80	
CAA GGA CTG AGG GCC ATG GAC ACG GGA CTC TAC ATC TGC AAG GTG GAG	288
Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu	
85 90 95	
CTC ATG TAC CCA CCG CCA TAC TAC CTG GGC ATA GGC AAC GGA ACC CAG	336
Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln	
100 105 110	
ATT TAT GTA ATT GAT CCA GAA CCG TGC CCA GAT TCT GAC TTC CTC CTC	384
Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Phe Leu Leu	
115 120 125	
TGG ATC CTT GCA GCA GTT AGT TCG GGG TTG TTT TTT TAT AGC TTT CTC	432
Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr Ser Phe Leu	
130 135 140	
CTC ACA GCT GTT TCT TTG AGC AAA ATG CTA AAG AAA AGA AGC CCT CTT	480
Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg Ser Pro Leu	
145 150 155 160	
ACA ACA GGG GTC TAT GTG AAA ATG CCC CCA ACA GAG CCA GAA TGT GAA	528
Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro Glu Cys Glu	
165 170 175	
AAG CAA TTT CAG CCT TAT TTT ATT CCC ATC AAT	561
Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn	
180 185	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly	
1 5 10 15	
Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu	
20 25 30	
Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val	

35	40	45
Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp		
50	55	60
Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile		
65	70	75
Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu		
85	90	95
Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln		
100	105	110
Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Phe Leu Leu		
115	120	125
Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr Ser Phe Leu		
130	135	140
Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg Ser Pro Leu		
145	150	155
Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro Glu Cys Glu		
165	170	175
Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn		
180	185	

- (2) INFORMATION FOR SEQ ID NO:15:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AATACGACTC ACTATAGG

18

- (2) INFORMATION FOR SEQ ID NO:16:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CACCACACTG TATTAACC

18

- (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
 1           5           10           15
Ala Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
          20           25           30
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
          35           40           45
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
          50           55           60
Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65           70           75           80
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
          85           90           95
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
          100          105          110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
          115          120          125
Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
          130          135          140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145          150          155          160
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
          165          170          175
Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
          180          185          190
Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
          195          200          205
Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
          210          215          220

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Met Ala Cys Leu Gly Leu Arg Arg Tyr Lys Ala Gln Leu Gln Leu Pro
 1           5           10           15
Ser Arg Thr Trp Pro Phe Val Ala Leu Leu Thr Leu Leu Phe Ile Pro
          20           25           30
Val Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val Tyr Leu Ala
          35           40           45

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Ser	Ser	His	Gly	Tyr	Ala	Ser	Phe	Pro	Cys	Glu	Tyr	Ser	Pro	Ser	His
50						55				60					
Asn	Thr	Asp	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Gln	Thr	Asn	Asp	Gln
65					70					75					80
Met	Thr	Glu	Val	Cys	Ala	Thr	Thr	Phe	Thr	Glu	Lys	Asn	Thr	Val	Gly
				85					90					95	
Phe	Leu	Asp	Tyr	Pro	Phe	Cys	Ser	Gly	Thr	Phe	Asn	Glu	Ser	Arg	Val
				100				105					110		
Asn	Leu	Thr	Ile	Gln	Gly	Leu	Arg	Ala	Val	Asp	Thr	Gly	Leu	Tyr	Leu
				115			120					125			
Cys	Lys	Val	Glu	Leu	Met	Tyr	Pro	Pro	Pro	Tyr	Phe	Val	Gly	Met	Gly
				130			135				140				
Asn	Gly	Thr	Gln	Ile	Tyr	Tyr	Ile	Asp	Pro	Glu	Pro	Cys	Pro	Asp	Ser
145				150						155					160
Asp	Phe	Leu	Leu	Trp	Ile	Leu	Tyr	Ala	Val	Ser	Leu	Gly	Leu	Phe	Phe
				165				170						175	
Tyr	Ser	Phe	Leu	Val	Ser	Ala	Val	Ser	Leu	Ser	Lys	Met	Leu	Lys	Lys
				180				185					190		
Arg	Ser	Pro	Leu	Thr	Thr	Gly	Val	Tyr	Val	Lys	Met	Pro	Pro	Thr	Glu
				195			200					205			
Pro	Glu	Cys	Glu	Lys	Gln	Phe	Gln	Pro	Tyr	Phe	Ile	Pro	Ile	Asn	
				210			215				220				

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Thr	Leu	Arg	Leu	Leu	Phe	Leu	Ala	Leu	Asn	Phe	Phe	Ser	Val	Gln
1				5				10						15	
Val	Thr	Glu	Asn	Lys	Ile	Leu	Val	Lys	Gln	Ser	Pro	Leu	Leu	Tyr	Val
			20					25					30		
Asp	Ser	Asn	Glu	Val	Ser	Leu	Ser	Cys	Arg	Tyr	Ser	Tyr	Asn	Leu	Leu
		35				40					45				
Ala	Lys	Glu	Phe	Arg	Ala	Ser	Leu	Tyr	Lys	Gly	Val	Asn	Ser	Asp	Val
		50				55				60					
Glu	Val	Cys	Val	Gly	Asn	Gly	Asn	Phe	Thr	Tyr	Gln	Pro	Gln	Phe	Arg
65				70				75						80	
Ser	Asn	Ala	Glu	Phe	Asn	Cys	Asp	Gly	Asp	Phe	Asp	Asn	Glu	Thr	Val
				85				90						95	
Thr	Phe	Arg	Leu	Trp	Asn	Leu	His	Val	Asn	His	Thr	Asp	Ile	Tyr	Phe
			100					105					110		
Cys	Lys	Ile	Glu	Phe	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Arg
		115				120						125			
Ser	Asn	Gly	Thr	Ile	Ile	His	Ile	Lys	Glu	Lys	His	Leu	Cys	His	Thr
		130				135					140				
Gln	Ser	Ser	Pro	Lys	Leu	Phe	Trp	Ala	Leu	Tyr	Val	Val	Ala	Gly	Val
145				150						155					160
Leu	Phe	Cys	Tyr	Gly	Leu	Leu	Val	Thr	Val	Ala	Leu	Cys	Val	Ile	Trp
				165				170						175	

Thr	Asn	Ser	Arg	Arg	Asn	Arg	Leu	Leu	Gln	Val	Thr	Tyr	Met	Asn	Met
			180					185					190		
Thr	Pro	Arg	Arg	Pro	Gly	Leu	Thr	Arg	Lys	Pro	Tyr	Gln	Pro	Tyr	Ala
		195					200					205			
Pro	Ala	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Pro						
	210					215									

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Thr	Leu	Arg	Leu	Leu	Phe	Leu	Ala	Leu	Ser	Phe	Phe	Ser	Val	Gln
1				5					10					15	
Val	Thr	Glu	Asn	Lys	Ile	Leu	Val	Lys	Gln	Ser	Pro	Leu	Leu	Val	Tyr
			20					25					30		
Asp	Asn	Asn	Glu	Val	Ser	Leu	Ser	Cys	Arg	Tyr	Ser	Tyr	Asn	Leu	Leu
		35					40					45			
Ala	Lys	Glu	Phe	Arg	Ala	Ser	Leu	Tyr	Lys	Gly	Val	Asn	Ser	Asp	Val
	50					55					60				
Glu	Val	Cys	Val	Gly	Asn	Gly	Asn	Phe	Thr	Tyr	Gln	Pro	Gln	Phe	Arg
65					70					75				80	
Pro	Asn	Val	Gly	Phe	Asn	Cys	Asp	Gly	Asn	Phe	Asp	Asn	Glu	Thr	Val
				85					90					95	
Thr	Phe	Arg	Leu	Trp	Asn	Leu	Asp	Val	Asn	His	Thr	Asp	Ile	Tyr	Phe
			100					105					110		
Cys	Lys	Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys
		115					120					125			
Ser	Asn	Gly	Thr	Ile	Ile	His	Ile	Lys	Glu	Lys	His	Leu	Cys	His	Ala
	130					135					140				
Gln	Thr	Ser	Pro	Lys	Leu	Phe	Trp	Pro	Leu	Val	Val	Val	Ala	Gly	Val
145					150					155					160
Leu	Leu	Cys	Tyr	Gly	Leu	Leu	Tyr	Thr	Val	Thr	Leu	Cys	Ile	Ile	Trp
				165					170					175	
Thr	Asn	Ser	Arg	Arg	Asn	Arg	Leu	Leu	Gln	Ser	Asp	Tyr	Met	Asn	Met
			180					185					190		
Thr	Pro	Arg	Arg	Leu	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala
		195					200					205			
Pro	Ala	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Pro						
	210					215									

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Leu	Arg	Leu	Leu	Leu	Ala	Leu	Asn	Leu	Phe	Pro	Ser	Ile	Gln	Val
1				5					10					15	
Thr	Gly	Asn	Lys	Ile	Leu	Val	Lys	Gln	Ser	Pro	Met	Leu	Val	Ala	Tyr
			20					25					30		
Asp	Asn	Ala	Tyr	Asn	Leu	Ser	Cys	Lys	Tyr	Ser	Tyr	Asn	Leu	Phe	Ser
		35					40					45			
Arg	Glu	Phe	Arg	Ala	Ser	Leu	His	Lys	Gly	Leu	Asp	Ser	Ala	Val	Glu
	50					55					60				
Val	Cys	Val	Val	Tyr	Gly	Asn	Tyr	Ser	Gln	Gln	Leu	Gln	Val	Tyr	Ser
65					70					75				80	
Lys	Thr	Gly	Phe	Asn	Cys	Asp	Gly	Lys	Leu	Gly	Asn	Glu	Ser	Val	Thr
				85					90					95	
Phe	Tyr	Leu	Gln	Asn	Leu	Tyr	Val	Asn	Gln	Thr	Asp	Ile	Tyr	Phe	Cys
			100					105					110		
Lys	Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser
		115					120					125			
Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro
	130					135					140				
Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly
145					150					155				160	
Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Tyr	Thr	Val	Ala	Phe	Ile	Ile
			165						170					175	
Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met
		180					185						190		
Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro
		195				200						205			
Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser				
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Leu	Gly	Ile	Leu	Val	Val	Leu	Cys	Leu	Ile	Pro	Ala	Ala	Asp	Val
1				5					10					15	
Thr	Glu	Asn	Lys	Ile	Leu	Val	Ala	Gln	Arg	Pro	Leu	Leu	Ile	Val	Ala
			20					25					30		
Asn	Arg	Thr	Ala	Thr	Leu	Val	Cys	Asn	Tyr	Thr	Tyr	Asn	Gly	Thr	Gly
		35					40					45			
Lys	Glu	Phe	Arg	Ala	Ser	Leu	His	Lys	Gly	Thr	Asp	Ser	Ala	Val	Glu
	50					55					60				
Val	Cys	Phe	Ile	Ser	Trp	Asn	Met	Thr	Lys	Ile	Asn	Ser	Asn	Ser	Asn
65					70					75				80	
Lys	Glu	Phe	Asn	Cys	Arg	Gly	Ile	His	Asp	Lys	Asp	Lys	Val	Ile	Phe
			85						90					95	

Asn	Leu	Trp	Asn	Met	Ser	Ala	Ser	Gln	Thr	Asp	Ile	Tyr	Phe	Cys	Lys
			100					105					110		
Ile	Glu	Ala	Met	Tyr	Pro	Pro	Pro	Tyr	Val	Tyr	Asn	Glu	Lys	Ser	Asn
		115					120					125			
Gly	Thr	Val	Ile	His	Tyr	Arg	Glu	Thr	Pro	Ile	Gln	Thr	Gln	Glu	Pro
		130				135					140				
Glu	Ser	Ala	Thr	Ser	Tyr	Trp	Val	Met	Tyr	Ala	Val	Thr	Gly	Leu	Leu
145					150					155					160
Gly	Phe	Tyr	Ser	Met	Leu	Ile	Thr	Ala	Val	Phe	Ile	Ile	Tyr	Arg	Gln
				165					170					175	
Lys	Ser	Lys	Arg	Asn	Arg	Tyr	Arg	Gln	Ser	Asp	Tyr	Met	Asn	Met	Thr
			180					185					190		
Pro	Arg	His	Pro	Pro	His	Gln	Lys	Asn	Lys	Gly	Tyr	Pro	Ser	Tyr	Ala
		195					200					205			
Pro	Thr	Arg	Asp	Tyr	Thr	Ala	Tyr	Arg	Ser	Trp	Gln	Pro			
	210					215					220				